RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/723,164_
Source: _1 FWO_
Date Processed by STIC: _11/18/04_

ENTERED

RAW SEQUENCE LISTING   DATE: 11/18/2004
PATENT APPLICATION: US/10/723,164   TIME: 09:31:36

Input Set : A:\66783-142.TXT
Output Set: N:\CRF4\11182004\J723164.raw

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 4 <110> APPLICANT: Targan, Stephan R.
 5         Vasiliauskas, Eric A.
 6         Mow, William S.
 7         Yang, Huiying
 8         Fleshner, Phillip R.
 9         Rotter, Jerome I.
11 <120> TITLE OF INVENTION: Methods of Assessing Crohn's Disease
12         Patient Phenotype by I2, OmpC and ASCA Serologic Response
16 <130> FILE REFERENCE: 66783-142
18 <140> CURRENT APPLICATION NUMBER: US 10/723,164
19 <141> CURRENT FILING DATE: 2003-11-26
21 <150> PRIOR APPLICATION NUMBER: US 10/413,501
22 <151> PRIOR FILING DATE: 2003-04-11
24 <160> NUMBER OF SEQ ID NOS: 22.
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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29 <211> LENGTH: 302
30 <212> TYPE: DNA
31 <213> ORGANISM: P. aeruginosa
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34 <221> NAME/KEY: CDS
35 <222> LOCATION: (2)...(301)
37 <400> SEQUENCE: 1
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40     1               5                  10                  15
42 ttc aag agc aag gat gag ata ttg cgt gcc gtg atg gag gaa acc atc   97
43 Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
44              20                  25                  30
46 cat tac aac acc gcg atg atg cgc gct tca ctg gag gag gcg agc acg   145
47 His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
48          35                  40                  45
50 gtg cgc gaa cgc gtg ctg gcg ctg atc cgc tgc gag ttg cag tcg atc   193
51 Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
52      50                  55                  60
54 atg ggc ggc agt ggc gag gcc atg gcg gtg ctg gtc tac gaa tgg cgc   241
55 Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
56   65                  70                  75                  80
58 tcg ctg tcg gcc gaa ggc cag gcg cac gtg ctg gcc ctg cgt gac gtg   289
59 Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
60                  85                  90                  95
62 tat gag cag atc t                                                 302
63 Tyr Glu Gln Ile
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 64                  100
 67 <210> SEQ ID NO: 2
 68 <211> LENGTH: 100
 69 <212> TYPE: PRT
 70 <213> ORGANISM: P. aeruginosa
 72 <400> SEQUENCE: 2
 73 Asp Leu Ala Ser Ala Val Gly Ile Gln Ser Gly Ser Ile Phe His His
 74 1               5                  10                  15
 75 Phe Lys Ser Lys Asp Glu Ile Leu Arg Ala Val Met Glu Glu Thr Ile
 76           20                  25                  30
 77 His Tyr Asn Thr Ala Met Met Arg Ala Ser Leu Glu Glu Ala Ser Thr
 78           35                  40                  45
 79 Val Arg Glu Arg Val Leu Ala Leu Ile Arg Cys Glu Leu Gln Ser Ile
 80       50                  55                  60
 81 Met Gly Gly Ser Gly Glu Ala Met Ala Val Leu Val Tyr Glu Trp Arg
 82 65                  70                  75                  80
 83 Ser Leu Ser Ala Glu Gly Gln Ala His Val Leu Ala Leu Arg Asp Val
 84               85                  90                  95
 85 Tyr Glu Gln Ile
 86              100
 89 <210> SEQ ID NO: 3
 90 <211> LENGTH: 494
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Homo sapiens
 94 <400> SEQUENCE: 3
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 96 tggctgagtg ccagacatct gagaaggccc tgctccggcg ccaggcctgt gcccgctggt 120
 97 gtctggcccg cagcctccgc aagcacttcc actccatccc gccagctgca ccgggtgagg 180
 98 ccaagagcgt gcatgccatg cccgggttca tctggctcat ccggagcctg tacgagatgc 240
 99 aggaggagcg gctggctcgg aaggctgcac gtggcctgaa tgttgggcac ctcaagttga 300
100 cattttgcag tgtgggcccc actgagtgtg ctgccctggc ctttgtgctg cagcacctcc 360
101 ggcggcccgt ggccctgcag ctggactaca actctgtggg tgacattggc ctggagcagc 420
102 tgctgccttg ccttggtgtc tgcaaggctc tgtagtgagt gttactgggc attgctgttc 480
103 aggtatgggg gagc                                              494
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106 <211> LENGTH: 494
107 <212> TYPE: DNA
108 <213> ORGANISM: Homo sapiens
110 <400> SEQUENCE: 4
111 gctcccccat acctgaacag caatgcccag taacactcac tacagagcct tgcagacacc 60
112 aaggcaaggc agcagctgct ccaggccaat gtcacccaca gagttgtagt ccagctgcag 120
113 ggccacgggc cgccggaggt gctgcagcac aaaggccagg gcagcacact cagtggggcc 180
114 cacactgcaa aatgtcaact tgaggtgccc aacattcagg ccacgtgcag ccttccgagc 240
115 cagccgctcc tcctgcatct cgtacaggct ccggatgagc cagatgaacc cgggcatggc 300
116 atgcacgctc ttggcctcac ccggtgcagc tggcgggatg gagtggaagt gcttgcggag 360
117 gctgcgggcc agacaccagc gggcacaggc ctggcgccgg agcagggcct tctcagatgt 420
118 ctggcactca gccagcaggc cccagtgctc ccgggacaac agccctgcca ggaaggctgc 480
119 tgtgatctga aggt                                              494
121 <210> SEQ ID NO: 5
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128 ctcttgaaat ccaatggtct tttttcctta ctccattgcc taacattgtg gggtagaaat 120
129 aaagttcaaa gaccttcaga actggccca gctcctccct cttcacctga tctccccaag 180
130 aaaactgcag gatagactct gaagcttacc tgagccacct caagctctgg tgatcaccca 240
131 aggcttcagc cagggcctgg gcccctcgt cacccactct gttgccccag aatctgaaaa 300
132 ggccaaaaga gtcaacagac agtgtcagtg agtacctgat atgtgttcta gacatgaact 360
133 aacagtcctc ctccctctgc agtcccagcc agaggggcag gaccactcaa tcccagagtg 420
134 gcctcactgg ggctcctggt cccagcaaag tggacctgcc tccatctttt gggtgggatg 480
135 gccaaactta acccaagagt tttcagtggc tttacattac agacttagag aatagtagag 540
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 540
140 <212> TYPE: DNA
141 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 6
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145 catcccaccc aaaagatgga ggcaggtcca ctttgctggg accaggagcc ccagtgaggc 120
146 cactctggga ttgagtggtc ctgcccctct ggctgggact gcagagggag gaggactgtt 180
147 agttcatgtc tagaacacat atcaggtact cactgacact gtctgttgac tcttttggcc 240
148 ttttcagatt ctggggcaac agagtgggtg acgagggggc ccaggccctg gctgaagcct 300
149 tgggtgatca ccagagcttg aggtggctca ggtaagcttc agagtctatc ctgcagtttt 360
150 cttggggaga tcaggtgaag agggaggagc tggggccagt tctgaaggtc tttgaacttt 420
151 atttctaccc cacaatgtta ggcaatggag taaggaaaaa agaccattgg atttcaagag 480
152 aggacactcg agtctttctg ggtgacttgg aaatgtccct tgtcctctca gggtttttgat 540
155 <210> SEQ ID NO: 7
156 <211> LENGTH: 541
157 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 7
161 tttaaaaatg aaatcattgc tccctactta aagaggtaaa gacttctttc ttagacagag  60
162 aatcagatcc ttcacatgca gaatcattct cactgaatgt cagaatcaga agggatcctc 120
163 aaaattctgc cattcctctc tcccgtcacc ccattttaca gatagaaaaa ctgaggttcg 180
164 gagagctaaa acaggcctgc ccaggggcct taccagactt ccaggatggt gtcattcctt 240
165 tcaaggggcc tgcaggaggg cttctgcccc taggtaggtg atgcagttat tggacaacct 300
166 ggaaaagaag atacaatggt gagcttcaag gattcttggt tttcctcttg aaactgtcca 360
167 gttaaagaga ctgcaggagt tagccagtct actgaagccc acctgtccct tagacacatc 420
168 ctgctcatgt ctgagattcc caatgagctc atcaacaaag gctcagtacc atcagtgaaa 480
169 tgtaaccgtc tctcttccat tcactagatg agtttatcaa attaagtagc cactcccta 540
170 g                                                                541
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173 <211> LENGTH: 541
174 <212> TYPE: DNA
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 8
178 ctaagggagt ggctacttaa tttgataaac tcatctagtg aatggaagag agacggttac  60
179 atttcactga tggtactgag cctttgttga tgagctcatt gggaatctca gacatgagca 120
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180 ggatgtgtct aagggacagg tgggcttcag tagactggct aactcctgca gtctctttaa 180
181 ctggacagtt tcaagaggaa aaccaagaat ccttgaagct caccattgta tcttcttttc 240
182 caggttgtcc aataactgca tcacctacct aggggcagaa gccctcctgc aggcccccttg 300
183 aaaggaatga caccatcctg gaagtctggt aaggcccctg ggcaggcctg ttttagctct 360
184 ccgaacctca gtttttctat ctgtaaaatg gggtgacggg agagaggaat ggcagaattt 420
185 tgaggatccc ttctgattct gacattcagt gagaatgatt ctgcatgtga aggatctgat 480
186 tctctgtcta agaaagaagt ctttacctct ttaagtaggg agcaatgatt tcatttttaa 540
187 a                                                                 541
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190 <211> LENGTH: 1101
191 <212> TYPE: DNA
192 <213> ORGANISM: E. coli
194 <220> FEATURE:
195 <221> NAME/KEY: CDS
196 <222> LOCATION: (1)...(1101)
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200 Met Lys Val Lys Val Leu Ser Leu Leu Val Pro Ala Leu Leu Val Ala
201  1               5                  10                  15
203 ggc gca gca aac gct gct gaa gtt tac aac aaa gac ggc aac aaa tta   96
204 Gly Ala Ala Asn Ala Ala Glu Val Tyr Asn Lys Asp Gly Asn Lys Leu
205                  20                  25                  30
207 gat ctg tac ggt aaa gta gac ggc ctg cac tat ttc tct gac aac aaa  144
208 Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
209              35                  40                  45
211 gat gta gat ggc gac cag acc tac atg cgt ctt ggc ttc aaa ggt gaa  192
212 Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
213          50                  55                  60
215 act cag gtt act gac cag ctg acc ggt tac ggc cag tgg gaa tat cag  240
216 Thr Gln Val Thr Asp Gln Leu Thr Gly Tyr Gly Gln Trp Glu Tyr Gln
217  65                  70                  75                  80
219 atc cag ggc aac agc gct gaa aac gaa aac aac tcc tgg acc cgt gtg  288
220 Ile Gln Gly Asn Ser Ala Glu Asn Glu Asn Asn Ser Trp Thr Arg Val
221                  85                  90                  95
223 gca ttc gca ggt ctg aaa ttc cag gat gtg ggt tct ttc gac tac ggt  336
224 Ala Phe Ala Gly Leu Lys Phe Gln Asp Val Gly Ser Phe Asp Tyr Gly
225                  100                 105                 110
227 cgt aac tac ggc gtt gtt tat gac gta act tcc tgg acc gac gta ctg  384
228 Arg Asn Tyr Gly Val Val Tyr Asp Val Thr Ser Trp Thr Asp Val Leu
229              115                 120                 125
231 cca gaa ttc ggt ggt gac acc tac ggt tct gac aac ttc atg cag cag  432
232 Pro Glu Phe Gly Gly Asp Thr Tyr Gly Ser Asp Asn Phe Met Gln Gln
233          130                 135                 140
235 cgt ggt aac ggc ttc gcg acc tac cgt aac act gac ttc ttc ggt ctg  480
236 Arg Gly Asn Gly Phe Ala Thr Tyr Arg Asn Thr Asp Phe Phe Gly Leu
237 145                 150                 155                 160
239 gtt gac ggc ctg aac ttt gct gtt cag tac cag ggt aaa aac ggc aac  528
240 Val Asp Gly Leu Asn Phe Ala Val Gln Tyr Gln Gly Lys Asn Gly Asn
241                  165                 170                 175
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243 cca tct ggt gaa ggc ttt act agt ggc gta act aac aac ggt cgt gac    576
244 Pro Ser Gly Glu Gly Phe Thr Ser Gly Val Thr Asn Asn Gly Arg Asp
245         180                 185                 190
247 gca ctg cgt caa aac ggc gac ggc gtc ggc ggt tct atc act tat gat    624
248 Ala Leu Arg Gln Asn Gly Asp Gly Val Gly Gly Ser Ile Thr Tyr Asp
249         195                 200                 205
251 tac gaa ggt ttc ggt atc ggt ggt gcg atc tcc agc tcc aaa cgt act    672
252 Tyr Glu Gly Phe Gly Ile Gly Gly Ala Ile Ser Ser Ser Lys Arg Thr
253     210                 215                 220
255 gat gct cag aac acc gct gct tac atc ggt aac ggc gac cgt gct gaa    720
256 Asp Ala Gln Asn Thr Ala Ala Tyr Ile Gly Asn Gly Asp Arg Ala Glu
257 225                 230                 235                 240
259 acc tac act ggt ggt ctg aaa tac gac gct aac aac atc tac ctg gct    768
260 Thr Tyr Thr Gly Gly Leu Lys Tyr Asp Ala Asn Asn Ile Tyr Leu Ala
261             245                 250                 255
263 gct cag tac acc cag acc tac aac gca act cgc gta ggt tcc ctg ggt    816
264 Ala Gln Tyr Thr Gln Thr Tyr Asn Ala Thr Arg Val Gly Ser Leu Gly
265             260                 265                 270
267 tgg gcg aac aaa gca cag aac ttc gaa gct gtt gct cag tac cag ttc    864
268 Trp Ala Asn Lys Ala Gln Asn Phe Glu Ala Val Ala Gln Tyr Gln Phe
269         275                 280                 285
271 gac ttc ggt ctg cgt ccg tcc ctg gct tac ctg cag tct aaa ggt aaa    912
272 Asp Phe Gly Leu Arg Pro Ser Leu Ala Tyr Leu Gln Ser Lys Gly Lys
273     290                 295                 300
275 aac ctg ggt cgt ggc tac gac gac gaa gat atc ctg aaa tat gtt gat    960
276 Asn Leu Gly Arg Gly Tyr Asp Asp Glu Asp Ile Leu Lys Tyr Val Asp
277 305                 310                 315                 320
279 gtt ggt gct acc tac tac ttc aac aaa aac atg tcc acc tac gtt gac   1008
280 Val Gly Ala Thr Tyr Tyr Phe Asn Lys Asn Met Ser Thr Tyr Val Asp
281             325                 330                 335
283 tac aaa atc aac ctg ctg gac gac aac cag ttc act cgt gac gct ggc   1056
284 Tyr Lys Ile Asn Leu Leu Asp Asp Asn Gln Phe Thr Arg Asp Ala Gly
285             340                 345                 350
287 atc aac act gat aac atc gta gct ctg ggt ctg gtt tac cag ttc       1101
288 Ile Asn Thr Asp Asn Ile Val Ala Leu Gly Leu Val Tyr Gln Phe
289             355                 360                 365
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294 <211> LENGTH: 367
295 <212> TYPE: PRT
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302             20                  25                  30
303 Asp Leu Tyr Gly Lys Val Asp Gly Leu His Tyr Phe Ser Asp Asn Lys
304         35                  40                  45
305 Asp Val Asp Gly Asp Gln Thr Tyr Met Arg Leu Gly Phe Lys Gly Glu
306     50                  55                  60
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